

Fig. 1-1

h: 1	MSGSTQPVAQTWRATEPRYPHSLSYVPVQIARTHTDVGLEYYQHHSRDYASHLSPGSI IQPQRRRPSLLSEFPQGNERSQELHLRPESHSYLPELGKSEM	-----A-----GI-----S-----P-----T-----S-----RTF-----PDI
m: 1		
h: 101	EFIESKRPRLELLPDLLRPSPLLATGQAGSEDLTKDRSLTGKLEPVSPSPHTDPELELVPPRLSKEELIQN.MDRVDTREITWVEQIISKLKKKQQQ	--T-----T-----S-----A-----A-----A-S-----RL-----
m: 101		
h: 200	LEEEAAKPEPEKPVSPPIESKHSRLVQIIYDENRKAEEAAHRILEGGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWEQKFC	-----T-----R-----
m: 201		
h: 300	QRYDQLMEAEWKVERIENPRRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQSGSLSMSPARSEHEVSEIIDGLSEQENLEKQMRQLAVIPMML	-----S-----A-----RHVV
m: 301		
h: 399	YDADQORIKFINNGLMADPMKVYKDRQVNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVAEVCVLYYYLTKKNNENYKSLVRRSYRRRGKSQQQQQQQ	-----D-----T-----RD-----
m: 401	RR	
h: 499	QQQQQQQQQPMRSSQEEKDEKEKEKEAEEKEEKEPVENDKEDLLKEKTDGSDNDEKEAVASKGRKTANSQGRKGRITRSMANEANSEEAITPQ	-----A-----E-----QDA-----E-E-S-----H--TA--
m: 500		
h: 599	QSAELASMELNBSRWTEEMETAKKGLLEHGRNWSAIFARMVGSKTVSOCKNFYFNYKKRONLDEILQHQHKLMBEKERNARRKKKAPAAAASEEAFFPV	-----M-----T-----A
m: 596		
m: -AC:	HQTPGPGARLLTQQELRAPIPSTPQLQPHSHRPHPSKEPCTPPCQSGPAGAHGLRSAPRKDSK*	
h: 699	VEDEEMEASGVTCNEEEMVEEAAT.....VNNSSDTESIPSPHTEAAKDTGQNGPKPPATLGCADGPPPGPPTPPPEDIPAPTESTP	
m: 696	A-----SA-----LA-----SQASGNEVPRVGCSGPAA-----V--RS--T-----G-EALPAATQP-VP--E-PAA--A-PS-	
h: 781	ASEATLAPTPPPAPPPSSPPVVPKKEKEEETAAPPVEEGEEQKPPAAEELAVDTGKAEEP.....VKSECTEEAAEEGPA.KGKDAEAAAEATAE	
m: 793	VPD-SGPPS-E-S-S-AA--AT-D-D-Q-APA-P--QT-DAK--SEAE...I-V-P--EASEEPPES---DHK--T--E-ED-A-GT--I-ITVS-	
h: 871	RALKAЕКEGGSGRATTAKSSGAPQDSDDSSATCSADEVDEAEGDGKNRLLSPPRSLLTFTGDPANASPOKPLDLKQLKQRAAAIPIQVTKVHEPPRED	
m: 889	AP--V-.EAGSAAV-KGS---T-----P-----G-----A--ST-----	

Fig. 1-2

MEAWDAHP -> (SMRT)

h: 971	AAPTKPAPPAPPPQNLQ	PESDAPQQPGSSPRGKSRSP	PAPPADKEAKPVFFP	AFAAEAQKLPDPPCWT	SGLPFFVPPREV	IKASPHADPDSAFS	YAPP
m: 987	TV-P-V-V-T-H	-G-VS-S-G	-V-E-A	-PT-G-SYRLS	-HA.GHR--	.SH-----	T-TR-.L---
h: 1071	GHPLPLGLHDTAR	PVLP RPPTISNPP	PLISSAKHPSVLER	QIGAI	SQGMVQLHVPYSE	HAKAPVGPVTMGLPL	PMDPKKLAPFSGVKQEQLSPRGQAGP
m: 1083	-----S	-----G	-----R-H	-----M-L-E	-AV-----	GTALAPPVEA	---ASQ..
h: 1171	PESLGVPTAQEASV	LRGTALGSVP	GGSI	TKGIPSTRVPS	DSAITYRGSITHG	TPADVLYKGTITRI	IGEDSPSRLDRGREDSLPKGHVIEGKKGHVLSY
m: 1179	Y-GC-R-QLQ	LYH....	PR-----	S-V-----	A-T-----	-----
h: 1271	EGGMSVTQCSKED	GRSSGPPHETA	APKRTYDMMEGR	VGRAISSASIEGL	MGRAIPPERHSP	PHLKEQHHRGSI	TQIGIPRSYVEAQEDYLRREAKLLKR
m: 1243	-----S	-----TVT	-----Q	-----	-----	-----	-----
h: 1371	EGTPPPPPSRDL	TEAYKTQ...	ALGPLKLKPAHE	GLVATVKEAGRS	THEIPREELR	HTPELPLAPRPL	KEGSITQGTPLKYDTGASTTGSKKHDVRSLLI
m: 1341	-----P	-----T--PR	PLDP	-----T--V	-----R	-----S--PS	-----T
h: 1468	GSPGRTFPPVH	PLDMADARAL	ERACYEESLKS	RPGTASSSGG	SIARGAPVIV	PELGKPRQSP	LTIEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSS
m: 1441	-----P--AL	-----I	-----S--S	-GA--T--V	-----TS	-----L	-----
h: 1568	KASQDRKLTST	PREIAKSPHST	VPEHHPHPI	SPYEHLLRGV	SGVDLYRSHI	PLAFDPTSI	PRGIPLD.AAAAAYLPRHLAPNPTYPHLYPPYLIRGYPDT
m: 1541	-----	-----T	-----G	-----EA	-----S	-----	-----

M->(TRAC1)

h: 1667	AALENRQTIINDYITSQQMHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPPTCTPATAMDRLAYLPTAPQPFSSRRHSSS
m: 1641	-----A-S-----S-----I-----P-----H-----
h: 1767	LSPGGPHLTKPTTTSSSERERDRDRDREREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRQTQDALQQRPS
m: 1741	-----A-A-----E-E-----G-----
h: 1867	VLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFTLAKPPARSGLPEPASSPS
m: 1825	-----S-VV-S--GT-----E-----TS-----V-G-----T-----
h: 1967	KGSEPRPLVPPVSGHATIARTPAKNLAPHHASDPAPPASADPHREKTQSKPFSIQELELRSLGYH.GSSYSPEGVEPVSPVSPSLTHDKGLPKHLE
m: 1922	-S-----S-A-S-S-TA-----S-----G-T--L-----S-AG--D--I-----S-P-----
h: 2066	ELDKSHLEGLRKPQPGVKLGCEAAHLPHLRPLBPESQSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPABLYSFPGASCPVLD
m: 2021	-----H-----M--SA-----I-----G-----
h: 2166	LRRPPDLXLPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGEDGIEPVSPPEGMTPEGHRSRAVYPLL YRDGEQTEPSRMGKSPGNTSQPPAFFSKL
m: 2121	-----T-----S-----SS-A-----A-----G-----
h: 2266	TESNSAMVSKKQEIINKLNTNHRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIRKALMGKYDQWEESPPLISANAFNPLNASA
m: 2220	-----G-----A-----C-----P-----G-----
h: 2366	SLP.AAMPITAADGRSDHTLTSPPGGGKAKVSGRBPSSRKAKSPAPGLASGDRPPSVSVHSEGCNRRRTPLTNRVWEDRPSAGSTFPYFNPLIMRLQAG
m: 2320	-----T-----A-----
h: 2465	VMASPPPPGLPAGSGPLAGPHHAWDEEPPKLLCSQVETLSDSE 2507
m: 2420	-----A-----2462

Fig. 3

